

Figure 1.

HSPDE1A	MGSSATEIEELENTTFKYLTGEQTEKMWQRLKGILRCLVKQLERGDV	
HSPDE1B	MELSPRSPPEMLEESDCPSPLELKSAPSKKMWIKLRSLLRYMVKQLENGEI	47
HSPDE1C	MESPTKEIEEFESNSLKYLQPEQIEKIWLRLRGLRKYKKTSQRLRSLVKQLERGEA	51
	*. :** : : * ::*::: * * :******:	56
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HSPDE1A	NVVDLKKNIEYAASVLEAVYIDETRRLLDTEDELSDIQTDSVPSEVRDWLASTFTRKMGM	107
HSPDE1B	NIEELKKNLEYTASLLEAVYIDETRQILDTEDELQELRSDAVPSEVRDWLASTFTQQARA	10/
HSPDE1C	SVVDLKKNLEYAATVLESVYIDETRRLLDTEDELSDIQSDAVPSEVRDWLASTFTRQMGM	
	:: :***:*:*::**:**:**:*******::::::::::	110
HSPDE1A	TKKKPEEKPKFRSIVHAVQAGIFVERMYRKTYHMVGLAYPAAVIVTLKDVDKWSFDVFAL	167
HSPDE1B	KGRRAEEKPKFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSL	171
HSPDE1C	MLRRSDEKPRFKSIVHAVQAGIFVERMYRRTSNMVGLSYPPAVIEALKDVDKWSFDVFSL	
	::.:***:*:***************	
HSPDE1A	NEASGEHSLKFMIYELFTRYDLINRFKIPVSCLITFAEALEVGYSKYKNPYHNLIHAADV	227
HSPDE1B	NQAADDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADV	231
HSPDE1C	NEASGDHALKFIFYELLTRYDLISRFKIPISALVSFVEALEVGYSKHKNPYHNLMHAADV	236
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UCDDD1		
HSPDE1A	TQTVHYIMLHTGIMHWLTELEILAMVFAAAIHDYEHTGTTNNFHIQTRSDVAIL YNDRSV	287
HSPDE1B	TQTVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHTGTTNSFHIQTKSECAIVYNDRSV	291
HSPDE1C	TQTVHYLLYKTGVANWLTELEIFAIIFSAAIHDYEHTGTTNNFHIQTRSDPAIL YNDRS V	296
	***** :: *** : *** : * * * * * * * * *	
HSPDE1A	LENDUNGS AVDI MORRE MALLI TAN GYDDUNDA DAN MARKE GERMANIA	
HSPDE1B	LENHHVSAAYRLMQEEE-MNILINLSKDDWRDLRNLVIEMVLSTDMSGHFQQIKNIRNSL	346
HSPDE1C	LENHHISSVFRLMQDDE-MNIFINLTKDEFVELRALVIEMVLATDMSCHFQQVKTMKTAL	350
	LENHHLSAAYRLLQDDEEMNILINLSKDDWREFRTLVIEMVMATDMSCHFQQIKAMKTAL	356
HSPDE1A	QQPEGIDRAKTMSLILHAADISHPAKSWKLHYRWTMALMEEFFLQGDKEAELGLPFSPLC	106
HSPDE1B	QQLERIDKPKALSLLLHAADISHPTKQWLVHSRWTKALMEEFFRQGDKEAELGLPFSPLC	410
HSPDE1C	QQPEAIEKPKALSLMLHTADISHPAKAWDLHHRWTMSLLEEFFRQGDREAELGLPFSPLC	416
	** * *: *: **: **: **: **: **: * * * *	410
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HSPDE1A	DRKSTMVAQSQIGFIDFIVEPTFSLLTDSTEKIVIPLIEEASKAETSSYVASS	459
HSPDE1B	DRTSTLVAQSQIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPS	466
HSPDE1C	DRKSTMVAQSQVGFIDFIVEPTFTVLTDMTEKIVSPLIDETSQTGGTGQRRSSLNSISSS	476
	.:*************	
HSPDE1A	CDETUCT IIT	
HSPDE1B	STTIVGLHIADALRRSNTKGSMSDGSYSPDYSLAAVDLKSFKNNL	504
HSPDE1C	LDVEVGDPNPDVVSFRSTWVKRIQENKQKWKERAASGITNQMS	509
"DI DIIIC	DAKRSGVKTSGSEGSAPINNSVISVDYKSFKATWTEVVHINRERWRAKVPKEEKAKKEAE	536
	*	
HSPDE1A	VDIIQQNKERWKELAAQEARTSSQKCEFIHQ	52 5
HSPDE1B	IDELSPCEEEAPPSPAEDEHNQNGNLD	535 536
HSPDE1C	EKARLAAEEQQKEMEAKSQAEEGASGKAEKKTSGETKNQVNGTRANKSDNPRGKNSKAEK	596
	· :*. :: ::	
HSPDE1A		
HSPDE1B		
HSPDE1C	SSGEQQQNGDFKDGKNKTDKKDHSNIGNDSKKTDDSQE 634	

Figure 2

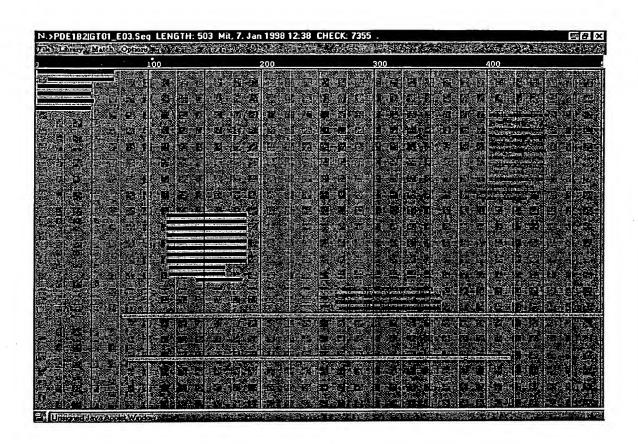




Figure 3

PDE 1A Subtypes

Bovine



Bovine



Human



Murine



Human



PDE1B1

Figure 4A N-terminal sequences of PDE1A splice variants 1 MGSSATEIEELENTT KYLTGEQTEKMWQRLKGILRCLVKQLER DVNVVDLKKNIEYAA PDE1A3 111141111111111111111111111111 MDDHVTIRKKHLQRPIFRLRCLVKQLERGDVNVVDLKKNIEYAA PDE1A5 Figure 4B N-terminal sequences of PDE1B splice variants 1 MELSPRSPPEMLEESDCPSPLELKSAPSKKMWIKLRSLLRYMVKOLENGEINIEELKKNL PDE1B1 PDE1B2 Figure 4C Comparison of the CaM binding domains of the PDE1A1 and PDE1B2 splice variants PDE1A1 MDDHVTIRRKHLQRPIFRLRCLVKQLEKGDVNVIDLKKN PDE1B2 Comparison of the CaM binding domains of the PDE1A2 Figure 4D and PDE1B1 splice variants. PDE1A2 1 MGSTATETEELENTTFKYLIGEQTEKMWQRLKGILRCLVKQLEKGDVNVIDLKKNIE

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1 MELSPRSPPEMLESDCPSPLELKSAPSKKMWIKLRSLLRYMVKQLENGEVNIEELKKNLE

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Figure 5

